

GenCore version 5.1.13  
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OM protein - protein search, using SW model

Run on: January 16, 2003 16:40:12 - Search time 43 7143 seconds  
(without alignments)  
56.562 Million cell updates/sec

Title: US-09-856-070-21

Perfect score: 60

Sequence: 1 BELMLRQDYEE 12

Scoring table: RLOSUM62

Gapop 10 0 , Gapext 0 5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organellae:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	60	100.0	586	4	Q96GUR	Q96GUR homo sapien
2	57	95.0	159	4	Q9UJZ6	Q9UJZ6 homo sapien
3	57	95.0	586	11	Q9DC11	Q9DC11 mys musculu
4	55	91.7	158	4	Q9UJZ7	Q9UJZ7 homo sapien
5	53	88.3	455	11	Q9VHK3	Q9VHK3 rattus norv
6	45	75.0	585	14	Q9VSW6	Q9VSW6 gallus gall
7	40	66.7	534	14	Q9QXY9	Q9QXY9 ligo rubrip
8	39	65.0	250	17	Q9HR00	Q9HR00 halobacteri
9	39	65.0	376	5	Q95QW7	Q95QW7 caenorhabdi
10	39	65.0	429	4	P78514	P78514 homo sapien
11	39	65.0	453	4	Q99854	Q99854 homo sapien
12	39	65.0	584	15	Q55449	Q55449 synectocyst
13	39	65.0	634	9	Q9XJ53	Q9XJ53 bacterioph
14	39	65.0	402	4	Q9YAW4	Q9YAW4 homo sapien
15	38	63.3	47	15	Q9VHK2	Q9VHK2 atidopsis
16	38	63.3	130	16	Q9K660	Q9K660 bacillus ha

Q8UHE2 agrobacteri	108	63.3	150	16	Q8UHE2
Q9SV18 macaca fasc	108	63.3	311	6	Q9SV18
Q9W20 macaca fasc	108	63.3	476	5	Q9W20
Q9M50 homo sapien	108	63.3	556	4	Q9M50
Q91480 salmo salar	108	63.3	1058	13	Q91480
Q8T517 anopheles q	108	63.3	1280	5	Q8T517
Q20766 caenorhabdi	108	63.3	1363	5	Q20766
Q64706 bacterioph	108	63.3	111	9	Q64706
Q34838 bacillus su	108	63.3	111	16	Q34838
Q45212 lucilia faja	108	63.3	125	7	Q45212
Q9UJZ8 homo sapien	108	63.3	156	4	Q9UJZ8
Q9W20 homo sapien	108	63.3	151	4	Q9W20
Q8T512 pyrococcus	108	63.3	217	17	Q8T512
Q8U0V8 pyrococcus	108	63.3	231	17	Q8U0V8
Q9V217 pyrococcus	108	63.3	281	17	Q9V217
Q8T9V0 adeles ae-qrp	108	63.3	292	5	Q8T9V0
Q52534 pseudomonas	108	63.3	306	2	Q52534
Q9P9S2 xylicella fas	108	63.3	321	16	Q9P9S2
Q66941 aquifex aco	108	63.3	337	16	Q66941
Q8T366 drosophila	108	63.3	418	5	Q8T366
Q9VFL8 drosophila	108	63.3	443	5	Q9VFL8
Q51748 xenopus lae	108	63.3	454	13	Q51748
Q8PH5 ectocarpus	108	63.3	465	12	Q8PH5
Q9VZ8 streptomyce	108	63.3	487	16	Q9VZ8
Q974U8 sulfobobus	108	63.3	249	17	Q974U8
Q8SV88 encephalito	108	63.3	248	5	Q8SV88
Q9H242 pseudomonas	108	63.3	253	15	Q9H242
Q9ZUUL arabidopsis	108	63.3	284	10	Q9ZUUL
P78849 schizosacch	108	63.3	327	3	P78849

ALIGNMENTS

RESULT 1

Q96GUR

ID Q96GUR PRELIMINARY; PRT; 586 AA.

AC Q96GUR: 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

OS Similar to villin 2 (ezrin).

OC Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=COLON;

RA Strausberg R.;

FI Submitted (SEP 2001) to the EMBL/GenBank/DBJ databases

DR EMBL: BC013903; AHI13903.1; -

DR InterPro: IPR000299; Band\_4.1.

DR InterPro: IPR000798; Pz/rad/moesin.

DR Pfam: PF00373; Band\_4.1; 1.

DR Pfam: PF00769; ERM; 1.

DR PROSITE: PS00660; BAND\_4.1; UNKNOWN\_1.

DR PROSITE: PS00661; BAND\_4.1.2; UNKNOWN\_1.

DR PROSITE: PS00057; BAND\_4.1.3; 1.

SD SEQUENCE 586 AA; F18592CF49A7CC46 CRC64;

Query Match

Best Local Similarity 100.0%; Score 60; DB 4; Length 586;

Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 BELMLRQDYEE 12

DB 345 BELMLRQDYEE 356

RESULT 2

Q9UJZ6

ID Q9UJZ6 PRELIMINARY; PRT; 159 AA.

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Q9UJZ6;
BI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fadiel A., Chen Z.C., Naftolin F.;
RT "Mutation of ezrin gene in cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189213; AAF03156.1; -.
DR InterPro: IPR000299; Hand.4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS00557; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 19234 MW; 7C398388B7HA70FA CRC64;

Query Match 95.0%; Score 57; DB 4; Length 159;
Best Local Similarity 91.7%; Pred. No. 0.011;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FELMLRLQDYVE 12
| | | | | | | | | |
DB 148 FELMLRLQDYED 159

RESULT 3
Q9DC11
ID Q9DC11 PRELIMINARY; PRI: 586 AA.
AC Q9DC11;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone:0610037B22, full insert sequence.
GN VIL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
KA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
KA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
KA Aizawa K., Izawa M., Nishi K., Niyosawa H., Kondo S., Yamana K.,
KA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
KA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
KA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
KA Kuchl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
KA Schiraldi L.M., Stambli F., Suzuki K., Tomita M., Wagner I., Washio T.,
KA Sakai K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,
KA Blake J., Bellelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
KA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
KA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
KA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
KA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
KA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-P.,
KA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
KA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
KA Bayashizaki Y.;
RI "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK012765; BAB2341.1; -.
DR MGI: MGI:98941; VIL2.
DR InterPro: IPR000249; Band_41.1.

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DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Band_41; 1.
DR PRINTS: PR00769; ERM; 1.
DR SMART: SM00295; H41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS00057; BAND_41_3; 1.
SQ SEQUENCE 586 AA; 69434 MW; 591A8F575F6DE3E CRC64;

Query Match 95.0%; Score 57; DB 11; Length 586;
Best Local Similarity 91.7%; Pred. No. 0.041;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FELMLRLQDYVE 12
| | | | | | | | | |
DB 345 FELMLRLQDYEQ 356

RESULT 4
Q9UJZ7
ID Q9UJZ7 PRELIMINARY; PRI: 158 AA.
AC Q9UJZ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen Z.C., Fadiel A., Naftolin F.;
RT "Ezrin gene mutation in ovarian cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188897; AAF03155.1; -.
DR InterPro: IPR000299; Hand.4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS00557; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA; 19086 MW; 86F92E1HC6F2957E CRC64;

Query Match 91.7%; Score 55; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FELMLRLQDYVE 11
| | | | | | | | | |
DB 148 FELMLRLQDYVE 158

RESULT 5
Q8VHK3
ID Q8VHK3 PRELIMINARY; PRI: 455 AA.
AC Q8VHK3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ezrin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SPRAGUE-DAWLEY;
RA Gunn Moore P.J., Tait S., Prophy P.J.;
PL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF450298; AAL47844.1; -.

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DR InterPro: IP000299; Rand\_41\_1  
 DR InterPro: IP000798; Ez/rad/moesin.  
 DR Pfam: PF00373; Band\_41; 1.  
 DR Pfam: PF00769; ERM; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR SMART: SM00295; B41; 1.  
 DR PROSITE: PS00660; RAND\_41\_1; UNKNOWN\_1.  
 DR PROSITE: PS00661; RAND\_41\_2; UNKNOWN\_1.  
 DR PROSITE: PS00557; BAND\_41\_3; 1.  
 FT NON\_TER 455 455  
 SQ SEQUENCE 455 AA; 54174 MW; 1FC9A95E47D6993 CRC64;

Query Match 88.3%; Score 53; DB 11; Length 455;  
 Best Local Similarity 83.3%; Pred. No. 0.17;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12  
 |||||  
 DB 345 EELMLRLQDYEE 356

RESULT 6

ID O9YCW6 PRELIMINARY; PRT; 585 AA.  
 AC O9YCW6;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Ezrin.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WHITE LPCROWN; TISSUE=BRAIN;  
 RX MEDLINE=99171943; PubMed=10051754;  
 RA Takahashi M., Yamada M., Noda M.;  
 RT "Specific expression of ezrin, a cytoskeletal membrane linker protein,  
 in a subset of chick retinotectal and sensory projections";  
 RL Eur J Neurosci 11:545-558(1999).  
 DR EMBL: AB019790; BAA75497.1; 1.  
 DR InterPro: IP000299; Band\_41.1.  
 DR InterPro: IP000798; Ez/rad/moesin.  
 DR Pfam: PF00373; Band\_41; 1.  
 DR Pfam: PF00769; ERM; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR SMART: SM00295; B41; 1.  
 DR PROSITE: PS00660; RAND\_41\_1; 1.  
 DR PROSITE: PS00661; RAND\_41\_2; 1.  
 DR PROSITE: PS00557; BAND\_41\_3; 1.  
 SQ SEQUENCE 585 AA; 65496 MW; 4547644EF740AEC CRC64;

Query Match 75.0%; Score 45; DB 13; Length 585;  
 Best Local Similarity 72.7%; Pred. No. 6.3;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 11  
 |||||  
 DB 345 EELMLRLQDYEE 355

RESULT 7

ID Q90XY5 PRELIMINARY; PRT; 534 AA.  
 AC Q90XY5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 60.2 kDa protein.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;  
 OC Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21455642; PubMed=11571655;  
 RA Yu W.P., Pallen C.J., Tay A., Jirik F.R., Brenner S., Iain Y.H.,  
 RA Venkatesh B.;  
 RT "Conserved synteny between the Fugu and human PTEN locus and the  
 PT evolutionary conservation of vertebrate PTEN function";  
 RL Oncogene 20:5554-5561(2001).  
 DR EMBL: AF25922; AA108420.1; 1.  
 DR PMR: AF25922; AA108420.1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 534 AA; 60250 MW; 850964074F8816 CRC64;

Query Match 66.7%; Score 40; DB 13; Length 534;  
 Best Local Similarity 58.3%; Pred. No. 47;  
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12  
 |||||  
 DB 35 EELMLRLQDYEE 46

RESULT 8

ID Q9HRO0 PRELIMINARY; PRT; 250 AA.  
 AC Q9HRO0;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Vng0546c.  
 GN VNG0546C.  
 GN VNG0546C.  
 OS Halobacterium sp. (strain NRC-1).  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
 OC Halobacteriaceae; Halobacterium.  
 OX NCBI\_TaxID=64091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=29594483; PubMed=11016950;  
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Herquist B., Pan M.,  
 RA Shukla H.D., Jasky S.K., Hallig N.S., Thorsson V., Sbrogna J.,  
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,  
 RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
 RA Maddecks D.G., Tablonski P.E., Krebs M.P., Angewine C.M., Dale H.,  
 RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.H.,  
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
 RA Ebbardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;  
 RT "Genome sequence of Halobacterium species NRC-1";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12175-12181(2000).  
 DR EMBL: AE005006; AB019068.1; 1.  
 DR InterPro: IP004426; Cons\_hypoth62.  
 DR InterPro: IP002766; DUF75.  
 DR InterPro: IP000508; SigPase.  
 DR Pfam: PF01908; DUF75; 1.  
 DR Pfam: PF008434; DUF75; 1.  
 DR TIGFAMS: TIGF00162; Cons\_hypoth62; 1.  
 DR PROSITE: PS00761; SPASE\_1\_3; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 250 AA; 26165 MW; 875A96708FCCF887 CRC64;

Query Match 65.8%; Score 39; DB 17; Length 250;  
 Best Local Similarity 66.7%; Pred. No. 33;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EELMLRLQDYEE 12  
 |||||  
 DB 226 EELMLRLQDYEE 237

RESULT 9

Q95QW7

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10 Q99QW7 PRELIMINARY; PRT; 376 AA.
AC Q99QW7;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DI 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Hypothetical 44.4 kDa protein.
GN C14F5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Polodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RC MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Mix P.;
RT "The sequence of C. elegans cosmid C14F5.3";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission. ";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: 029682; AAC02434.1; -.
KW Hypothetical protein.
SQ SEQUENCE 376 AA; 44436 MW; 93B32C5H13C4A6CE CRC64;

Query Match 65.0%; Score 39; DB 5; Length 376;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 12
II :|||||
1b 92 EEQAKLQVEE 103

RESULT 10
P78514 PRELIMINARY; PRT; 429 AA.
AC P78514; Q99B44;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DI 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DE 01-MAY-1997 (TEMBLrel. 03, Last annotation update)
DE Hypothetical 46.1 kDa protein (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Keen T.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: 085995; AAB61919.1; -.
DR EMBL: 085994; AAB61918.1; -.
DR EMBL: 085997; AAB46606.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 429 AA; 48092 MW; D8E2471A95971E9A CRC64.

Query Match 65.0%; Score 39; DB 4; Length 429;
Best Local Similarity 72.7%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ELMRLQDYEE 12

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II:|||||
Db 157 ELILRLQVEE 167

RESULT 11
Q99854 PRELIMINARY; PRT; 453 AA.
AC Q99854;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DI 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Hypothetical 51.1 kDa protein (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA Keen T.J.;
RL Submited (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: 087408; AAB47568.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 453 AA; 51050 MW; C5F53EE64A841418 CRC64;

Query Match 65.0%; Score 39; DB 4; Length 453;
Best Local Similarity 72.7%; Pred. No. 60;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ELMRLQDYEE 12
II:|||||
1b 181 ELILRLQVEE 191

RESULT 12
Q55449 PRELIMINARY; PRT; 584 AA.
AC Q55449;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DI 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Hypothetical protein slr0031.
GN SLR0031.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC 6803;
RA Tabata S.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome. ";
RL DNA Res. 2:153-166(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=97061201; PubMed=8905211;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hikosawa M., Sugita M., Sasaki S., Kimura T.,
RA Hosouchi T., Matsuoka A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein coding regions. ";

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RL DNA Res. 3:109-136(1996).  
 DR EMBL: D64006; BAAL0791.1; -  
 DR MROPS; M61.001; -  
 DR InterPro: IPR001478; P0V.  
 DR InterPro: IPR001330; Zn\_Mtpeptdse.  
 DR Pfam: PF00595; PDZ; 1  
 DR SMART: SM00228; PDZ; 1  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 534 AA; 60866 MW; 808100664.4284AF GC64;

Query Match 65.0%; Score 39; DB 16; Length 584;  
 Best Local Similarity 63.6%; Pred. No. 78;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Caps 0;

QY 1 EELMLRLQDYEE 11  
 I:|||||  
 Db 521 EQLSLRLKDYQ 531

## RESULT 13

Q9XJS3 PRELIMINARY; PROT; 634 AA.

AC Q9XJS3;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Putative replication initiation protein p12.  
 OS Bacteriophage PM2.  
 OS Bacteriophage PM2.  
 OC Viruses; dsDNA viruses, no RNA stage; Corticoviridae; Corticovirus.  
 NCBI\_TaxID=10661;  
 [1]  
 SEQUENCE FROM N.A.  
 RA Kivela H.M., Mannisto R.H., Kalkkinnen N., Hamford J.K.H.;  
 "Purification and protein composition of PM2, the first lipid-  
 containing bacterial virus to be isolated.";  
 RL Virology 0:0-0(1999)  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99434236; PubMed=10502514;  
 RA Mannisto R.H., Kivela H.M., Paulin L., Hamford J.K.H.;  
 "The complete genome sequence of PM2, the first lipid containing  
 bacterial virus to be isolated.";  
 RL Virology 262:355-363(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Mannisto R.H., Kivela H.M., Paulin L., Hamford J.K.H.;  
 Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases  
 DR EMBL: AF155037; AAD43543.1; -  
 SQ SEQUENCE 634 AA; 72094 MW; 856100004FEB2506 GC64;

Query Match 65.0%; Score 39; DB 9; Length 634;  
 Best Local Similarity 63.6%; Pred. No. 85;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Caps 0;

QY 2 EELMLRLQDYEE 12  
 I:|||||  
 Db 275 FIMVRLPYGVEE 285

## RESULT 14

Q9Y699 PRELIMINARY; PROT; 802 AA.

AC Q9Y699;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE PM2-responsive osteosarcoma B1 protein.  
 GN B1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;

RL SEQUENCE FROM N.A.  
 RP TISSUE=OSTEOSARCOMA;  
 RX MEDLINE=99234731; PubMed=10221542;  
 RA Adams A.F., Koserblatt M., Suva L.J.;  
 "Identification of a novel parathyroid hormone-responsive gene in  
 human osteoblastic cells.";  
 RL Bone 24:385-313(1999).  
 DR EMBL: AF095771; AAD25981.1; -  
 SQ SEQUENCE 802 AA; 89244 MW; 30785443234CA32 GC64;

Query Match 55.0%; Score 39; DB 4; Length 802;  
 Best Local Similarity 72.7%; Pred. No. 114+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Caps 0;

QY 2 EELMLRLQDYEE 12  
 I:|||||  
 Db 530 EELMLRLQDYEE 540

## RESULT 15

Q9C6K2 PRELIMINARY; PROT; 86 AA.

AC Q9C6K2;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Hypothetical 10.0 kDa protein.  
 GN P8A12.1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Cuscuta; Brassicales; Brassicaceae; Arabidopsi.  
 NCBI\_TaxID=3702;  
 [1]  
 SEQUENCE FROM N.A.  
 RP STRAIN=CV\_ COLUMBIA;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 White B., Alonso J., Altieri D., Araujo R., Bowman C.L., Brooks S.Y.,  
 Bucher E., Chan A., Chao Q., Chen H., Chou K.F., Chin C.W.,  
 Chua M.K., Dunn L., Gonyer A.B., Gonyer A.E., Gonyer T.B., Gonyer K.,  
 Dunn P., Elqu P., Feldblum T.V., Feng J.-D., Feng B., Fujii C.Y.,  
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 Hunter J.R., Jenkins J., Johnson-Hopson C., Khan S., Khaykin R.,  
 Kim C.J., Koo H., Kremenetskaia I., Kurtz D.H., Kwan A., Lam B.,  
 Langin Hooper S., Lee A., Lee J.M., Lee C.A., Li J.H., Li Y.-P.,  
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,  
 Millischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 Faj G., Petrotou E., Plam F.K., Rhee M., Rooney T., Rowley D.,  
 Sakano H., Salzman S., Schwartz J.P., Shinn P., Southwick A.M.,  
 Subramaniam S., Tarr P., Tarr P., Town C.D.,  
 Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,  
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana.";  
 RL Nature 408:816-820(2000)  
 DR EMBL: AC09284; AAC50944.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 86 AA; 10022 MW; 0FFLE869423EB84B GC64;

Query Match 63.3%; Score 48; DB 10; Length 86;  
 Best Local Similarity 58.3%; Pred. No. 17;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Caps 0;

QY 1 EELMLRLQDYEE 12  
 I:|||||  
 Db 67 EDVMLPKEDYGE 78

Search completed: January 16, 2003, 16:55:44  
 Job time : 44.7143 secs

